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(21) International Application Number: <b>PCT/US97/06020</b> (22) International Filing Date: <b>11 April 1997 (11.04.97)</b>  (71) Applicant ( <i>for all designated States except US</i> ): <b>HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).</b>  (72) Inventors; and (75) Inventors/Applicants ( <i>for US only</i> ): <b>OLSEN, Henrik, S. [DK/US]; 182 Kendrick Place #24, Gaithersburg, MD 20878 (US). LI, Haodong [CN/US]; 11033 Rutledge Drive, Gaithersburg, MD 20878 (US).</b>  (74) Agents: <b>BROOKES, A., Anders et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).</b>		(81) Designated States: <b>AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</b>  Published <i>With international search report.</i> <i>With an indication in relation to deposited biological material furnished under Rule 13bis separately from the description.</i>	
(54) Title: <b>EXTRACELLULAR/EPIDERMAL GROWTH FACTOR LIKE PROTEIN</b>			
(57) Abstract			
<p>The present invention discloses extracellular/epidermal growth factor polypeptides and polynucleotides encoding such polypeptides. Also provided is a procedure for producing such polypeptides by recombinant techniques and therapeutic uses of the polypeptides which include induction of DNA synthesis, stimulating wound healing, treating neurological disorders, treating ocular disorders, treating kidney and liver disorders and stimulating embryogenesis and angiogenesis. Also disclosed are antagonists against such polypeptide and their use as a therapeutic to treat neoplasia. Also disclosed are diagnostic assays for detecting altered levels of the polypeptide of the present invention and mutations in the nucleic acid sequences which encode the polypeptides of the present invention.</p>			

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**EXTRACELLULAR/EPIDERMAL GROWTH FACTOR LIKE PROTEIN*****Field of the Invention***

10 This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the use of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides. The polypeptide of the present invention has been putatively identified as a human extracellular protein-like/Epidermal Growth Factor-like protein, hereafter referred to as "EEGF". The invention also relates to inhibiting the action  
15 of such polypeptides.

***Background of the Invention***

Cellular growth and differentiation appear to be initiated, promoted, maintained and regulated by a multiplicity of stimulatory, inhibitory and synergistic factors and hormones. The  
20 alteration and/or breakdown of the cellular homeostasis mechanism seems to be a fundamental cause of growth related diseases, including neoplasia. Growth modulatory factors are implicated in a wide variety of pathological and physiological processes including signal transduction, cell communication, growth and development, embryogenesis, immune response, hematopoiesis, cell survival and differentiation, inflammation, tissue repair and remodeling,  
25 atherosclerosis and cancer. Epidermal growth factor (EGF), transforming growth factor alpha (TGF $\alpha$ ), betacellulin, amphiregulin, and vaccinia growth factor among other factors are growth and differentiation modulatory proteins produced by a variety of cell types either under normal physiological conditions or in response to exogenous stimuli and are members of the EGF family.

30

These peptide growth factors influence epithelial and epidermal cells through autocrine and paracrine mechanisms. They also play important roles in normal wound healing in tissues such as skin, cornea and gastrointestinal tract and all share substantial amino acid sequence homology including the conserved placement of three intra-chain disulfide bonds. In addition, all the factors of this family bind to a 170,000 molecular weight transmembrane glycoprotein receptor and activate the tyrosine kinase activity in the receptor's cytoplasmic domain (Buhrow, S.A. et al., *J. Bio. Chem.*, 258:7824-7826(1983)).

The receptors are expressed by many types of cells including skin keratinocytes, fibroblasts, vascular endothelial cells, and epithelial cells of the gastro-intestinal tract (GI) tract.

These peptide growth factors are synthesized by several cells involved in wound healing including platelets, keratinocytes, and activated macrophages. These growth factors have also been implicated in both the stimulation of growth and differentiation of certain cells, for example, neoplasia, and the inhibition of other types of cells.

Betacellulin is a 32-kilodalton glycoprotein that appears to be processed from a larger transmembrane precursor by proteolytic cleavage. The carboxyl-terminal domain of betacellulin has 50% sequence similarity with that of rat transforming growth factor α. Betacellulin is a potent mitogen for retinal pigment epithelial cells and vascular smooth muscle cells.

Amphiregulin is a bifunctional cell growth regulatory factor which exhibits potent inhibitory activity on DNA synthesis in neoplastic cells, yet promotes the growth of certain normal cells. A wide variety of uses for amphiregulin have been assigned including the treatment of wounds and cancers. For example, amphiregulin has potent anti-proliferative effects in vitro on several human cancer cell lines of epithelial origin. Amphiregulin also induces the proliferation of human foreskin fibroblasts as shown in United States Patent Application No. 5,115,096.

TGFα has pleiotropic biological effects. The production of certain members of TGFα is synthesized by a number of oncogenically transformed fibroblasts (Ciardiello et al., *J. Cell. Biochem.*, 42:45-57 (1990)), as well as by a variety of tumors, including renal, breast and squamous carcinomas, melanomas and glioblastomas (Deryck, R. et al., *Cancer Res.*, 47:707-712 (1987)). There is direct evidence that TGFα expression can be a contributing factor in the

conversion of a normal cell to its tumorigenic counterpart by analyzing transgenic mice in which tumor cells express high levels of TGF $\alpha$ . TGF $\alpha$  transgenic animals display a variety of neoplastic lesions, depending on the strain of mouse and the choice of promotor regulating TGF $\alpha$  expression (Sandgren, et al., *Cell*, 61:1121-1135 (1990)).

5        TGF $\alpha$  also plays a role in normal embryonic development and adult physiology (Derynck, R. *Adv. Cancer Res.*, 58:27-5 (1992)). TGF $\alpha$  has been expressed in many tissues including skin, brain, gastrointestinal mucosa and activating macrophages. Accordingly, TGF $\alpha$  is an important factor in controlling growth of epithelial cells and has a role in wound healing. TGF $\alpha$  has also been found to be angiogenic (Schreiber, et al., *Science*, 232:1250-1253 (1986)).

10      The polypeptide of the present invention has been putatively identified as an Extracellular/Epidermal Growth Factor. This identification has been made as a result of amino acid sequence homology to human extracellular protein which is a secreted protein with EGF-like domains that is abundant in heart tissue.

#### Summary of the Invention

15      In accordance with one aspect of the present invention, there are provided novel full-length and mature EEGF polypeptides, as well as biologically active and diagnostically or therapeutically useful fragments, analogs and derivatives thereof. The polypeptides of the present invention are of human origin.

20      In accordance with another aspect of the present invention, there are provided isolated nucleic acid molecules encoding the EEGF polypeptides of the present invention, including mRNAs, cDNAs, genomic DNAs as well as analogs and biologically active and diagnostically or therapeutically useful fragments thereof.

25      In accordance with another aspect of the present invention there is provided an isolated nucleic acid molecule encoding a mature polypeptide expressed by the human cDNA contained in ATCC Deposit No. \_\_\_\_\_.

In accordance with another aspect of the present invention there is provided an isolated nucleic acid molecule encoding a polypeptide expressed by the human cDNA contained in ATCC Deposit No. 97285.

30      In accordance with yet a further aspect of the present invention, there are provided processes for producing such polypeptide by recombinant techniques comprising culturing

recombinant prokaryotic and/or eukaryotic host cells, containing a nucleic acid sequence encoding a polypeptide of the present invention.

In accordance with yet a further aspect of the present invention, there are provided processes for utilizing such polypeptides, or polynucleotides encoding such polypeptides for therapeutic purposes, for example, to regulate vascular smooth muscle cell proliferation, to treat Marfan syndrome, to stimulate wound healing, to restore normal neurological functioning after trauma or AIDS dementia, to treat ocular disorders, to treat kidney and liver disorders, to promote hair follicular development, to stimulate growth and differentiation of various epidermal and epithelial cells *in vivo* and *in vitro* and for the treatment of burns, ulcers and corneal incisions, to stimulate embryogenesis.

In accordance with yet a further aspect of the present invention, there is also provided nucleic acid probes comprising nucleic acid molecules of sufficient length to specifically hybridize to nucleic acid sequences of the present invention.

In accordance with yet a further aspect of the present invention, there are provided antibodies against such polypeptides.

In accordance with yet a further aspect of the present invention, there are provided agonists to the polypeptide of the present invention.

In accordance with yet another aspect of the present invention, there are provided antagonists to such polypeptides, which may be used to inhibit the action of such polypeptides, for example, in the treatment of corneal inflammation, neoplasia, for example, tumors and cancers and for psoriasis.

In accordance with still another aspect of the present invention, there are provided diagnostic assays for detecting diseases related to overexpression of the polypeptide of the present invention and mutations in the nucleic acid sequences encoding such polypeptide.

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing such polypeptides, or polynucleotides encoding such polypeptides, for *in vitro* purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors.

These and other aspects of the present invention should be apparent to those skilled in the art from the teachings herein.

#### **Brief Description of the Drawings**

The following drawings are illustrative of embodiments of the invention and are not meant to limit the scope of the invention as encompassed by the claims.

Figure 1 depicts the cDNA sequence (SEQ ID NO:1) and corresponding deduced amino acid sequence (SEQ ID NO:2) of EEGF. Both the standard one letter and three letter abbreviations for amino acids are used. The leader sequence is underlined and the five EGF repeats are delineated.

Figure 2 is an illustration of comparative amino acid sequence homology between the carboxyl terminal 392 amino acids of the polypeptide of the present invention (lower line) (amino acids 57-448 in SEQ ID NO:2) and human extracellular protein (upper line) (SEQ ID NO:9).

Figure 3 shows an alignment of an EGF domain of TGF- $\beta$ 1 (SEQ ID NO:10), an EGF domain of fibulin ("FBL" SEQ ID NO:11) and the five EGF domains of the EEGF polypeptide of the present invention shown in Figure 1 (EGF-1 comprises amino acids 112-153 of SEQ ID NO:2; EGF-2 comprises amino acids 154-190 of SEQ ID NO:2; EGF-3 comprises amino acids 191-230 of SEQ ID NO:2; EGF-4 comprises amino acids 231-271 of SEQ ID NO:2; and EGF-5 comprises amino acids 272-314 of SEQ ID NO:2).

#### Detailed Description of the Invention

In accordance with an aspect of the present invention, there is provided an isolated nucleic acid (polynucleotide) which encodes for the full-length and mature EEGF polypeptides having the deduced amino acid sequences of Figure 1 (SEQ ID NO:2).

A polynucleotide encoding a polypeptide of the present invention may be obtained from human heart, human brain and early stage brain tissue. The polynucleotide of this invention was discovered in a human fetal heart cDNA library. Its translation product has homology to the characteristic EGF domains. As shown in Figures 1 and 3, EEGF has five repeating EGF domains (EGF-1 comprises amino acids 112-153 of SEQ ID NO:2; EGF-2 comprises amino acids 154-190 of SEQ ID NO:2; EGF-3 comprises amino acids 191-230 of SEQ ID NO:2; EGF-4 comprises amino acids 231-271 of SEQ ID NO:2; and EGF-5 comprises amino acids 272-314 of SEQ ID NO:2) with strong homology between themselves and with other members of the EGF family. *See, for example, Lecka-Czernik, et al., Molecular and Cellular Biology, 15(1):120 (1995), and in particular the consensus EGF domain shown in Figure 5C on page 125.* The polynucleotide contains an open reading frame encoding a complete EEGF

polypeptide of 448 amino acids. EEGF exhibits a high degree of homology at the amino acid level to human extracellular protein with 45% identity and 34% similarity over a 392 amino acid stretch (as shown in Figure 2). Northern blot analysis of this protein shows high levels of expression in heart tissue with the transcript being approximately 2 kb.

5 In accordance with another aspect of the present invention there are provided isolated polynucleotides encoding a full-length and mature polypeptide expressed by the human cDNAs contained in ATCC Deposit No. \_\_\_\_\_, deposited with the American Type Culture Collection, 12301 Park Lawn Drive, Rockville, Maryland 20852, USA, on \_\_\_\_\_. The deposited cDNA material is contained in a pBluescript plasmid (Stratagene, La Jolla CA) which can be transformed into a

10 viable host such as XL-1 Blue.

All deposit(s) of EEGF cDNAs disclosed herein have been made under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for purposes of Patent Procedure. The strain will be irrevocably and without restriction or condition released to the public upon the issuance of a patent. These deposits are provided

15 merely as convenience to those of skill in the art and are not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained in the deposited materials, as well as the amino acid sequence of the polypeptides encoded thereby, are controlling in the event of any conflict with any description of sequences herein. A license may be required to make, use or sell the deposited materials, and no such license is hereby granted.

20 References to "polynucleotides" throughout this specification includes the DNA of the deposit referred to above.

The polynucleotide of the present invention may be in the form of RNA or in the form of DNA, which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. The coding sequence which encodes the mature polypeptide may be identical to the coding sequence shown in Figure 1 (SEQ ID NO:1) or may be a different coding sequence which coding sequence, as a result of the redundancy or degeneracy of the genetic code, encodes the same mature polypeptide as the DNA of Figure 1 (SEQ ID NO:1).

The polynucleotide which encodes for the mature polypeptide of Figure 1 (SEQ ID NO:2) may comprise, but is not limited to: nucleotide sequence coding for the mature polypeptide as shown in SEQ ID NO:2 as amino acids 26-448 or as encoded by the cDNA

contained in ATCC Deposit No. \_\_\_\_\_; the coding sequence for the mature polypeptide and additional coding sequence such as a leader or secretory sequence or a proprotein sequence; the coding sequence for the mature polypeptide (and optionally additional coding sequence) and non-coding sequence, such as introns or non-coding sequence 5' and/or 3' 5 of the coding sequence for the mature polypeptide.

Thus, the term "polynucleotide encoding a polypeptide" encompasses a polynucleotide which includes only coding sequence for the polypeptide as well as a polynucleotide which includes additional coding and/or non-coding sequence.

The present invention further relates to variants of the hereinabove described 10 polynucleotides which encode for fragments, analogs and derivatives of the polypeptide having the deduced amino acid sequence of Figure 1 (SEQ ID NO:2). The variant of the polynucleotide may be a naturally occurring allelic variant of the polynucleotide or a non-naturally occurring variant of the polynucleotide.

Thus, the present invention includes polynucleotides encoding the same mature 15 polypeptide as shown in Figure 1 (SEQ ID NO:2) as well as variants of such polynucleotides which variants encode for a fragment, derivative or analog of the polypeptide of Figure 1 (SEQ ID NO:2). Such nucleotide variants include deletion variants, substitution variants and addition or insertion variants.

As hereinabove indicated, the polynucleotide may have a coding sequence which is a 20 naturally occurring allelic variant of the coding sequence shown in Figure 1 (SEQ ID NO:1). As known in the art, an allelic variant is an alternate form of a polynucleotide sequence which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded polypeptide.

The present invention also includes polynucleotides, wherein the coding sequence for 25 the mature polypeptide may be fused in the same reading frame to a polynucleotide sequence which aids in expression and secretion of a polypeptide from a host cell, for example, a leader sequence which functions as a secretory sequence for controlling transport of a polypeptide from the cell. The polypeptide having a leader sequence is a preprotein and may have the leader sequence cleaved by the host cell to form the mature form of the polypeptide. The 30 polynucleotides may also encode for a proprotein which is the mature protein plus additional 5' amino acid residues. A mature protein having a prosequence is a proprotein and is an inactive

form of the protein. Once the prosequence is cleaved an active mature protein remains. Thus, for example, the polynucleotide of the present invention may encode for a mature protein, or for a protein having a prosequence or for a protein having both a prosequence and a presequence (leader sequence).

5       The polynucleotides of the present invention may also have the coding sequence fused in frame to a marker sequence which allows for purification of the polypeptide of the present invention. The marker sequence may be a hexa-histidine tag supplied by a pQE-9 vector to provide for purification of the mature polypeptide fused to the marker in the case of a bacterial host, or, for example, the marker sequence may be a hemagglutinin (HA) tag when a 10 mammalian host, e.g. COS-7 cells, is used. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson, I., et al., Cell, 37:767 (1984)).

The term "gene" means the segment of DNA involved in producing a polypeptide chain; it includes regions preceding and following the coding region (leader and trailer) as well as intervening sequences (introns) between individual coding segments (exons).

15     Fragments of the full length EEGF gene may be used as a hybridization probe for a cDNA library to isolate the full length gene and to isolate other genes which have a high sequence similarity to the gene or similar biological activity. Probes of this type preferably have at least 30 bases and may contain, for example, 50 or more bases. The probe may also be used to identify a cDNA clone corresponding to a full length transcript and a genomic clone or 20 clones that contain the complete EEGF gene including regulatory and promotor regions, exons, and introns. An example of a screen comprises isolating the coding region of the gene by using the known DNA sequence to synthesize an oligonucleotide probe. Labeled oligonucleotides having a sequence complementary to that of the gene of the present invention are used to screen a library of human cDNA, genomic DNA or mRNA to determine which members of the library 25 the probe hybridizes to.

The present invention further relates to polynucleotides which hybridize to the hereinabove-described sequences if there is at least 70%, preferably at least 90%, and more preferably at least 95%, 96%, 97%, 98% or 99% identity between the sequences. The present invention particularly relates to polynucleotides which hybridize under stringent conditions to 30 the hereinabove-described polynucleotides. As herein used, the term "stringent conditions" means hybridization will occur only if there is at least 95% and preferably at least 97% identity

between the sequences. The polynucleotides which hybridize to the hereinabove described polynucleotides in a preferred embodiment encode polypeptides which either retain substantially the same biological function or activity as the mature polypeptide encoded by the cDNAs of Figure 1 (SEQ ID NO:1). Such biological activity is known in the art and can be assayed by techniques known in the art. Particularly preferred techniques for assaying activity of a polypeptide of the invention include the EGF Receptor binding assays disclosed in Heath, et al., (1986) Proc. Natl. Acad. Sci. U.S.A. 83:6367 and Tam, et al., (1986) Proc. Natl. Acad. Sci. U.S.A. 83:8082, both of which are incorporated herein by reference.

Alternatively, the polynucleotide may have at least 15 bases, preferably at least 30 bases, and more preferably at least 50 bases which hybridize to a polynucleotide of the present invention and which has an identity thereto, as hereinabove described, and which may or may not retain activity. For example, such polynucleotides may be employed as probes for the polynucleotide of SEQ ID NO:1, for example, for recovery of the polynucleotide or as a diagnostic probe or as a PCR primer.

Thus, the present invention is directed to polynucleotides having at least a 70% identity, preferably at least 90% and more preferably at least a 95%, 96%, 97%, 98%, or 99% identity to a polynucleotide which encodes the polypeptide of SEQ ID NO:2 and polynucleotides complementary thereto as well as portions thereof, which portions have at least 15 consecutive bases preferably at least 30 consecutive bases and preferably at least 50 consecutive bases and to polypeptides encoded by such polynucleotides.

The present invention further relates to a polypeptide which has the deduced amino acid sequence of Figure 1 (SEQ ID NO:2), as well as fragments, analogs and derivatives of such polypeptide.

The terms "fragment," "derivative" and "analog" when referring to the polypeptide of Figure 1 (SEQ ID NO:2), means a polypeptide which retains essentially the same biological function or activity as such polypeptide. Thus, an analog includes a proprotein which can be activated by cleavage of the proprotein portion to produce an active mature polypeptide.

The polypeptide of the present invention may be a recombinant polypeptide, a natural polypeptide or a synthetic polypeptide, preferably a recombinant polypeptide.

The fragment, derivative or analog of the polypeptide of Figure 1 (SEQ ID NO:2) may be (i) one in which one or more of the amino acid residues are substituted with a conserved or

- non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the mature polypeptide is fused with another compound, such as a compound to increase  
5 the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the mature polypeptide, such as a leader or secretory sequence or a sequence which is employed for purification of the mature polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.
- 10 Preferred EEGF polypeptides are those comprising one or more of the EEGF EGF domains. Such domains are shown in Figure 1 (SEQ ID NO:2) as follows: EGF-1 comprises amino acids 112-153 of SEQ ID NO:2; EGF-2 comprises amino acids 154-190 of SEQ ID NO:2; EGF-3 comprises amino acids 191-230 of SEQ ID NO:2; EGF-4 comprises amino acids 231-271 of SEQ ID NO:2; and EGF-5 comprises amino acids 272-314 of SEQ ID NO:2.  
15 Polynucleotides encoding such polypeptides are also provided.

A particularly preferred EEGF polypeptide of the invention includes amino acids 57-448 of SEQ ID NO:2 or the polypeptide encoded by the cDNA contained in ATCC Deposit No. 97285. Polynucleotides encoding this preferred polypeptide are also provided.

The polypeptides and polynucleotides of the present invention are preferably provided  
20 in an isolated form, and preferably are purified to homogeneity.

The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the  
25 natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

The polypeptides of the present invention include the polypeptide of SEQ ID NO:2 (in particular the mature polypeptide) as well as polypeptides which have at least 70% similarity  
30 (preferably at least 70% identity) to the polypeptide of SEQ ID NO:2 and more preferably at least 90% similarity (more preferably at least 90% identity) to the polypeptide of SEQ ID NO:2

and still more preferably at least 95% similarity (still more preferably at least 95%, 96%, 97%, 98%, or 99% identity) to the polypeptide of SEQ ID NO:2 and also include portions of such polypeptides with such portion of the polypeptide generally containing at least 30 amino acids and more preferably at least 50 amino acids.

5 As known in the art "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide.

10 Fragments or portions of the polypeptides of the present invention may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, the fragments may be employed as intermediates for producing the full-length polypeptides. Fragments or portions of the polynucleotides of the present invention may be used to synthesize full-length polynucleotides of the present invention.

15 The present invention also relates to vectors which include polynucleotides of the present invention, host cells which are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques.

20 Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the present invention. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

25 The polynucleotides of the present invention may be employed for producing polypeptides by recombinant techniques. Thus, for example, the polynucleotide may be included in any one of a variety of expression vectors for expressing a polypeptide. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. However, any other vector may be used as long as it is replicable and 30 viable in the host.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Such procedures and others are deemed to be within the scope of those skilled in the art.

- 5       The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the E. coli lac or trp, the phage lambda P<sub>L</sub> promoter and other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses. The expression vector also contains a  
10      ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in E. coli.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as E. coli, Streptomyces, Salmonella typhimurium; fungal cells, such as yeast; insect cells such as Drosophila S2 and Spodoptera Sf9; animal cells such as CHO, COS or Bowes melanoma; adenoviruses; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example; Bacterial: pQE70, pQE60, pQE-9 (Qiagen), pBS, pD10, phagescript, psiX174,

pbluescript SK, pbsks, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia); Eukaryotic: pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.

5 Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P<sub>R</sub>, P<sub>L</sub> and trp. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of  
10 the appropriate vector and promoter is well within the level of ordinary skill in the art.

In a further embodiment, the present invention relates to host cells containing the above-described constructs. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (Davis, L., Dibner, M., Battey, J., *Basic Methods in Molecular Biology*, (1986)).  
15

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

20 Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold  
25 Spring Harbor, N.Y., (1989), the disclosure of which is hereby incorporated by reference.

Transcription of the DNA encoding the polypeptides of the present invention by higher eukaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp that act on a promoter to increase its transcription. Examples including the SV40 enhancer on the late side of the replication origin bp  
30 100 to 270, a cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from 5 operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), α-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a 10 fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or 15 more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include E. coli, Bacillus subtilis, Salmonella typhimurium and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but nonlimiting example, useful expression vectors for bacterial use 20 can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM1 (Promega Biotec, Madison, WI, USA). These 25 pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, 30 and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, such methods are well known to those skilled in the art.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell, 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

The polypeptides can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The polypeptides of the present invention may be a naturally purified product, or a product of chemical synthetic procedures, or produced by recombinant techniques from a prokaryotic or eukaryotic host (for example, by bacterial, yeast, higher plant, insect and mammalian cells in culture). Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. Polypeptides of the invention may also include an initial methionine amino acid residue.

The polynucleotides and polypeptides of the present invention may be employed as research reagents and materials for discovery of treatments and diagnostics for human disease.

The polypeptide of the present invention may be employed to regulate vascular smooth muscle cell proliferation.

The polypeptide of the present invention may also be employed for characterization of receptors. The EGF family of receptors currently includes four EGF receptors, denoted as EGFR1, EGFR2, EGFR3 and EGFR4. The EGFR2 receptor may also be referred to as ERB-2 and this molecule is useful for a variety of diagnostic and therapeutic indications (Prigent, S.A., 5 and Lemoine, N.R., Prog Growth Factor Res., 4:1-24 (1992)). The EEGF polypeptide is likely a ligand for one or more of these receptors as well as for an unidentified new EGF-type receptor. Use of the EEGF can assist with the identification, characterization and cloning of such receptors. For example, the EGF receptor gene represents the cellular homolog of the v-erb-B oncogene of avian erythroblastosis virus. Over expression of the EGF-receptor or 10 deletion of kinase regulatory segments of the protein can bring about tumorigenic transformation of cells (Manjusri, D. et al., Human Cytokines, 364 and 381 (1991)).

The polypeptides of the present invention may also be employed for restoration or enhancement of neurological functions diminished as a result of trauma or other damaging pathologies (such as AIDS dementia, senile dementia, etc). TGF $\alpha$  and its homologs have been 15 found to be the most abundant ligand for the EGF/TGF $\alpha$  receptor in most parts of the brain (Kaser, et al., Mol Brain Res. 16:316-322, (1992)). EEGF or soluble form thereof may also be employed to treat ocular disorders, for example, corneal inflammation. A variety of experiments have implicated members of the TGF $\alpha$  gene family in such pathologies. A recent paper summarizes some of the data related to the role these growth factors play in eye disease 20 (Mann, et al, Cell, 73:249-261 (1993)). Recent experiments have shown that a number of mice lacking the TGF $\alpha$  gene displayed corneal inflammation due to an infiltration of leukocytes and other cells to the substantia propria of the eyes.

In addition, the specificity of certain growth factors for their target cells can be exploited as a mechanism to destroy the target cell. For example, EEGF or soluble forms thereof can be 25 coupled, by a wide variety of methods known in the art, to toxic molecules: for example, a radiopharmaceutical which inactivate target cells. These growth factor-toxin fusions kill the target cell (and in certain cases neighboring cells by a variety of "bystander" effects). A recent example of such toxin-fusion genes is published by Mesri, et al., J. Biol. Chem. 268:4853-62 (1993). EEGF and related molecules may also be encapsulated in liposomes and may be 30 conjugated to antibodies which recognize and bind to tumor or cell specific antigens, thereby provided a means for "targeting" cells.

The EEGF polypeptide may also be employed to treat certain kidney disorders, since it has been found that there has been expression of these growth factors in the kidney. Thus, these factors may be necessary for the proper physiological maintenance of this organ. Treatments may also be related to liver regeneration or liver dysfunction.

5 A significant treatment involving EEGF relates to wound healing. The compositions of the present invention may be employed for treating a wide variety of wounds including substantially all cutaneous wounds, corneal wounds, and injuries to the epithelial-lined hollow organs of the body. Wounds suitable for treatment include those resulting from trauma such as burns, abrasions and cuts, as well as from surgical procedures such as surgical incisions and  
10 skin grafting. Other conditions suitable for treatment with the polypeptide of the present invention include chronic conditions, such as chronic ulcers, diabetic ulcers, other non-healing (trophic) conditions, to treat Marfan syndrome, to promote hair follicular development, to stimulate growth and differentiation of various epidermal and epithelial cells *in vivo* and *in vitro* and to stimulate embryogenesis.

15 EEGF or soluble fragment thereof may be incorporated in physiologically-acceptable carriers for application to the affected area. The nature of the carriers may vary widely and will depend on the intended location of application. For application to the skin, a cream or ointment base is usually preferred; suitable bases include lanolin, Silvadene (Marion) (particularly for the treatment of burns), Aquaphor (Duke Laboratories, South Norwalk, Conn.), and the like. If  
20 desired, it will be possible to incorporate EEGF containing compositions in bandages and other wound dressings to provide for continuous exposure of the wound to the peptide. Aerosol applications may also find use.

25 The concentration of EEGF in the treatment composition is not critical but should be enough to induce epithelial cell proliferation. The compositions may be applied topically to the affected area, typically as eye drops to the eye or as creams, ointments or lotions to the skin. In the case of the eyes, frequent treatment is desirable, usually being applied at intervals of 4 hours or less. On the skin, it is desirable to continually maintain the treatment composition on the affected area during the healing, with applications of the treatment composition from two to four times a day or more frequently.

30 The amount employed of the subject polypeptide will vary with the manner of administration, the employment of other active compounds, and the like, generally being in the

range of about 1 mg to 100 mg. The subject polypeptide may be employed with a physiologically acceptable carrier, such as saline, phosphate-buffered saline, or the like. The amount of compound employed will be determined empirically, based on the response of cells in vitro and response of experimental animals to the subject polypeptides or formulations containing the subject polypeptides.

The EEGF or soluble fragment thereof may be employed in the modulation of angiogenesis, bone resorption, immune response, and synaptic and neuronal effector functions. EEGF may also be used in the modulation of the arachidonic acid cascade.

Applications are also related to alopecia, hair loss and to other skin conditions which affect hair follicular development. Several lines of evidence implicate the involvement of growth factors in such conditions. As described above, "knockout" mice engineered to contain a null mutation in the TGF $\alpha$  gene display abnormalities related to quantitative and qualitative hair synthesis. In addition, mapping studies in mice have shown that some mutations affecting hair growth map to the TGF $\alpha$  gene locus (Mann et al, Cell, 73:249-261(1993)). Topical or systemic applications of EEGF or derivatives thereof may be employed to treat some forms of alopecia and hair loss and these claims fall within the scope of this invention.

Certain disease pathologies may be partially or completely ameliorated by the systemic clinical administration of the EEGF growth factor. This administration can be in the form of gene therapy (see below); or through the administration of peptides or proteins synthesized from recombinant constructs of EEGF DNA or from peptide chemical synthesis (Woo, et al., Protein Engineering 3:29-37 (1989).

This invention provides a method for identification of EEGF receptors. The gene encoding a receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting (Coligan, et al., Current Protocols in Immun., 1(2), Chapter 5, (1991)). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to EEGF, and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to EEGF. Transfected cells which are grown on glass slides are exposed to labeled EEGF, which can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-

transfected using an iterative sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor. As an alternative approach for receptor identification, labeled ligand can be photoaffinity linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the ligand-receptor can be excised, resolved into peptide fragments, and subjected to protein microsequencing. The amino acid sequence obtained from microsequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

This invention also provides a method of screening compounds to identify antagonist compounds to the polypeptide of the present invention. As an example, a mammalian cell or membrane preparation expressing a EEGF receptor is incubated with EEGF and a potential antagonist compound and the ability of the compound to inhibit a second signal from the receptor is measured to determine if it is an effective antagonist. Such second messenger systems include but are not limited to, cAMP guanylate cyclase, ion channels or phosphoinositidehydrolysis.

Another assay for identifying potential antagonists specific to the receptors to the polypeptide of the present invention is a competition assay which comprises isolating plasma membranes which over-express a receptor to the polypeptide of the present invention, for example, human A431 carcinoma cells. Serially diluted test sample in a medium (volume is approximately 10 microliters) containing 10 nM <sup>125</sup>I-EEGF is added to five micrograms of the plasma membrane in the presence of the potential antagonist compound and incubated for 4 hours at 4°C. The reaction mixtures are diluted and immediately passed through a millipore filter. The filters are then rapidly washed and the bound radioactivity is measured in a gamma counter. The amount of bound EEGF is then measured. A control assay is also performed in the absence of the compound to determine if the antagonists reduce the amount of bound EEGF.

Potential antagonist compounds include an antibody, or in some cases, an oligopeptide, which binds to the polypeptide. Alternatively, a potential antagonist may be a closely related protein which binds to the receptor which is an inactive forms of the polypeptide and thereby prevent the action of the polypeptide of the present invention.

Another antagonist compound is an antisense construct prepared using antisense technology. Antisense technology can be used to control gene expression through triple-helix

formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes for the mature polypeptides of the present invention, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA 5 oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix -see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al, Science, 241:456 (1988); and Dervan et al., Science, 251: 1360 (1991)), thereby preventing transcription and the production of the polypeptide of the present invention. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA 10 molecule into the polypeptide of the present invention (Antisense - Okano, J. Neurochem., 56:560 (1991); Oligodeoxynucleotides Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the polypeptide of the present invention.

15 Antagonist compounds include a small molecule which binds to the polypeptide of the present invention and blocks its action at the receptor such that normal biological activity is prevented. The small molecules may also bind the receptor to the polypeptide to prevent binding. Examples of small molecules include but are not limited to small peptides or peptide-like molecules.

20 The antagonists may be employed to treat neoplasia, for example, cancers and tumors. It is known that inhibition of secretion or production of members of the EGF family by tumor cells in mice causes regression of tumors, since these proteins stimulate induction of DNA synthesis in all cells including neoplastic cells.

The antagonists to the polypeptides of the present invention may also be used 25 therapeutically for the treatment of certain skin disorders, for example, psoriasis. Elevated levels of expression of members of this family of growth factors in skin biopsies taken from diseases such as psoriatic lesions have been found to be elevated (Cook, et al., Cancer Research, 52:3224-3227 (1992)). The antagonists may be employed in a composition with a pharmaceutically acceptable carrier, e.g., as hereinafter described.

30 The polypeptides of the present invention or agonist or antagonist compounds may be employed in combination with a suitable pharmaceutical carrier. Such compositions comprise a

therapeutically effective amount of the polypeptide or compound, and a pharmaceutically acceptable carrier or excipient. Such a carrier includes but is not limited to saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The formulation should suit the mode of administration.

5       The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human 10 administration. In addition, the polypeptides or compounds of the present invention may be employed in conjunction with other therapeutic compounds.

15      The pharmaceutical compositions may be administered in a convenient manner such as by the oral, topical, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes. The pharmaceutical compositions are administered in an amount which is effective for treating and/or prophylaxis of the specific indication. In general, they are 20 administered in an amount of at least about 10 mg/kg body weight and in most cases they will be administered in an amount not in excess of about 8 mg/Kg body weight per day. In most cases, the dosage is from about 10 mg/kg to about 1 mg/kg body weight daily, taking into account the routes of administration, symptoms, etc.

25      The polypeptides, and agonists and antagonists which are polypeptides, may also be employed in accordance with the present invention by expression of such polypeptides *in vivo*, which is often referred to as "gene therapy."

Thus, for example, cells from a patient may be engineered with a polynucleotide (DNA or RNA) encoding a polypeptide *ex vivo*, with the engineered cells then being provided to a 25 patient to be treated with the polypeptide. Such methods are well-known in the art and are apparent from the teachings herein. For example, cells may be engineered by the use of a retroviral plasmid vector containing RNA encoding a polypeptide of the present invention.

30      Similarly, cells may be engineered *in vivo* for expression of a polypeptide *in vivo* by, for example, procedures known in the art. For example, a packaging cell is transduced with a retroviral plasmid vector containing RNA encoding a polypeptide of the present invention such that the packaging cell now produces infectious viral particles containing the gene of interest.

These producer cells may be administered to a patient for engineering cells *in vivo* and expression of the polypeptide *in vivo*. These and other methods for administering a polypeptide of the present invention by such method should be apparent to those skilled in the art from the teachings of the present invention.

5        Retroviruses from which the retroviral plasmid vectors hereinabove mentioned may be derived include, but are not limited to, Moloney Murine Leukemia Virus, spleen necrosis virus, retroviruses such as Rous Sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, gibbon ape leukemia virus, human immunodeficiency virus, adenovirus, Myeloproliferative Sarcoma Virus, and mammary tumor virus. In one embodiment, the retroviral plasmid vector is derived  
10      from Moloney Murine Leukemia Virus.

The vector includes one or more promoters. Suitable promoters which may be employed include, but are not limited to, the retroviral LTR; the SV40 promoter; and the human cytomegalovirus(CMV) promoter described in Miller, et al., Biotechniques Vol. 7, No. 9, 980-990 (1989), or any other promoter (e.g., cellular promoters such as eukaryotic cellular  
15      promoters including, but not limited to, the histone, pol III, and b-actin promoters). Other viral promoters which may be employed include, but are not limited to, adenovirus promoters, thymidine kinase (TK) promoters, and B19 parvovirus promoters. The selection of a suitable promoter will be apparent to those skilled in the art from the teachings contained herein.

20      The nucleic acid sequence encoding the polypeptide of the present invention is under the control of a suitable promoter. Suitable promoters which may be employed include, but are not limited to, adenoviral promoters, such as the adenoviral major late promoter; or heterologous promoters, such as the cytomegalovirus(CMV) promoter; the respiratory syncytial virus (RSV) promoter; inducible promoters, such as the MMT promoter, the metallothionein promoter; heat shock promoters; the albumin promoter; the ApoAI promoter; human globin promoters; viral  
25      thymidine kinase promoters, such as the Herpes Simplex thymidine kinase promoter; retroviral LTRs (including the modified retroviral LTRs hereinabove described); the b-actin promoter; and human growth hormone promoters. The promoter also may be the native promoter which controls the gene encoding the polypeptide.

30      The retroviral plasmid vector is employed to transduce packaging cell lines to form producer cell lines. Examples of packaging cells which may be transfected include, but are not limited to, the PES01, PA317, y-2, y-AM, PA12, T19-14X, VT-19-17-H2, yCRE, yCRIP,

GP+E-86, GP+envAm12, and DAN cell lines as described in Miller, Human Gene Therapy, Vol. 1, pgs. 5-14 (1990), which is incorporated herein by reference in its entirety. The vector may transduce the packaging cells through any means known in the art. Such means include, but are not limited to, electroporation, the use of liposomes, and CaPO<sub>4</sub> precipitation. In one alternative, the retroviral plasmid vector may be encapsulated into a liposome, or coupled to a lipid, and then administered to a host.

The producer cell line generates infectious retroviral vector particles which include the nucleic acid sequence(s) encoding the polypeptides. Such retroviral vector particles then may be employed, to transduce eukaryotic cells, either *in vitro* or *in vivo*. The transduced eukaryotic cells will express the nucleic acid sequence(s) encoding the polypeptide. Eukaryotic cells which may be transduced include, but are not limited to, embryonic stem cells, embryonic carcinoma cells, as well as hematopoietic stem cells, hepatocytes, fibroblasts, myoblasts, keratinocytes, endothelial cells, and bronchial epithelial cells.

This invention is also related to the use of the gene of the present invention as a diagnostic. Detection of a mutated form of the gene of the present invention will allow a diagnosis of a disease or a susceptibility to a disease which results from underexpression of the polypeptide of the present invention, for example, improper wound healing, improper neurological functioning, ocular disorders, kidney and liver disorders, hair follicular development, angiogenesis and embryogenesis.

Individuals carrying mutations in the human gene of the present invention may be detected at the DNA level by a variety of techniques. Nucleic acids for diagnosis may be obtained from a patient's cells, such as from blood, urine, saliva, tissue biopsy and autopsy material. The genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR (Saiki *et al.*, Nature, 324:163-166 (1986)) prior to analysis. RNA or cDNA may also be used for the same purpose. As an example, PCR primers complementary to the nucleic acid encoding a polypeptide of the present invention can be used to identify and analyze mutations thereof. For example, deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype. Point mutations can be identified by hybridizing amplified DNA to radiolabeled RNA or alternatively, radiolabeled antisense DNA sequences. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase A digestion or by differences in melting temperatures.

Sequence differences between the reference gene and genes having mutations may be revealed by the direct DNA sequencing method. In addition, cloned DNA segments may be employed as probes to detect specific DNA segments. The sensitivity of this method is greatly enhanced when combined with PCR. For example, a sequencing primer is used with double-stranded PCR product or a single-stranded template molecule generated by a modified PCR. The sequence determination is performed by conventional procedures with radiolabeled nucleotide or by automatic sequencing procedures with fluorescent-tags.

Genetic testing based on DNA sequence differences may be achieved by detection of alteration in electrophoretic mobility of DNA fragments in gels with or without denaturing agents. Small sequence deletions and insertions can be visualized by high resolution gel electrophoresis. DNA fragments of different sequences may be distinguished on denaturing formamide gradient gels in which the mobilities of different DNA fragments are retarded in the gel at different positions according to their specific melting or partial melting temperatures (see, e.g., Myers *et al.*, *Science*, 230:1242 (1985)).

Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and S1 protection or the chemical cleavage method (e.g., Cotton *et al.*, *PNAS, USA*, 85:4397-4401 (1985)).

Thus, the detection of a specific DNA sequence may be achieved by methods such as hybridization, RNase protection, chemical cleavage, direct DNA sequencing or the use of restriction enzymes, (e.g., Restriction Fragment Length Polymorphisms (RFLP)) and Southern blotting of genomic DNA.

In addition to more conventional gel-electrophoresis and DNA sequencing, mutations can also be detected by *in situ* analysis.

The present invention also relates to diagnostic assays for detecting altered levels of the polypeptide of the present invention in various tissues since an over-expression of the proteins compared to normal control tissue samples can detect the presence of certain disease conditions such as neoplasia, skin disorders, ocular disorders and inflammation. Assays used to detect levels of the polypeptide of the present invention in a sample derived from a host are well-known to those of skill in the art and include radioimmunoassays, competitive-binding assays, Western Blot analysis and preferably an ELISA assay. An ELISA assay initially comprises preparing an antibody specific to an antigen of the polypeptide of the present invention,

preferably a monoclonal antibody. In addition a reporter antibody is prepared against the monoclonal antibody. To the reporter antibody is attached a detectable reagent such as radioactivity, fluorescence or in this example a horseradish peroxidase enzyme. A sample is now removed from a host and incubated on a solid support, e.g. a polystyrene dish, that binds  
5 the proteins in the sample. Any free protein binding sites on the dish are then covered by incubating with a non-specific protein such as bovine serum albumin. Next, the monoclonal antibody is incubated in the dish during which time the monoclonal antibodies attach to any polypeptides of the present invention attached to the polystyrene dish. All unbound monoclonal antibody is washed out with buffer. The reporter antibody linked to horseradish peroxidase is  
10 now placed in the dish resulting in binding of the reporter antibody to any monoclonal antibody bound to polypeptides of the present invention. Unattached reporter antibody is then washed out. Peroxidase substrates are then added to the dish and the amount of color developed in a given time period is a measurement of the amount of protein present in a given volume of patient sample when compared against a standard curve.

15       A competition assay may also be employed to determine levels of the polypeptide of the present invention in a sample derived from the hosts. Such an assay comprises isolating plasma membranes which over-express the receptor for the polypeptide of the present invention. A test sample containing the polypeptides of the present invention which have been labeled, are then added to the plasma membranes and then incubated for a set period of time. Also added to the  
20 reaction mixture is a sample derived from a host which is suspected of containing the polypeptide of the present invention. The reaction mixtures are then passed through a filter which is rapidly washed and the bound radioactivity is then measured to determine the amount of competition for the receptors and therefore the amount of the polypeptides of the present invention in the sample.

25       Antibodies specific to EEGF may be used for cancer diagnosis and therapy, since many types of cancer cells up-regulate various members of the TGF $\alpha$  family during the process of neoplasia or hyperplasia. These antibodies bind to and inactivate EEGF. Monoclonal antibodies against EEGF (and/or its family members) are in clinical use for both the diagnosis and therapy of certain disorders including (but not limited to) hyperplastic and neoplastic growth abnormalities. Upregulation of growth factor expression by neoplastic tissues forms the basis for a variety of serum assays which detect increases in growth factor in the blood of  
30

affected patients. These assays are typically applied not only in diagnostic settings, but are applied in prognostic settings as well (to detect the presence of occult tumor cells following surgery, chemotherapy, etc).

In addition, malignant cells expressing the EEGF receptor may be detected by using 5 labeled EEGF in a receptor binding assay, or by the use of antibodies to the EEGF receptor itself. Cells may be distinguished in accordance with the presence and density of receptors for EEGF, thereby providing a means for predicting the susceptibility of such cells to the biological activities of EEGF.

The sequences of the present invention are also valuable for chromosome identification. 10 The sequence is specifically targeted to and can hybridize with a particular location on an individual human chromosome. Moreover, there is a current need for identifying particular sites on the chromosome. Few chromosome marking reagents based on actual sequence data (repeat polymorphisms) are presently available for marking chromosomal location. The mapping of 15 DNAs to chromosomes according to the present invention is an important first step in correlating those sequences with genes associated with disease.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the cDNA. Computer analysis of the 3' untranslated region of the gene is used to rapidly select primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers are then used for PCR screening of 20 somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the primer will yield an amplified fragment.

PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular DNA to a particular chromosome. Using the present invention with the same oligonucleotide primers, sublocalization can be achieved with panels of fragments from specific chromosomes 25 or pools of large genomic clones in an analogous manner. Other mapping strategies that can similarly be used to map to its chromosome include *in situ* hybridization, prescreening with labeled flow-sorted chromosomes and preselection by hybridization to construct chromosome specific-cDNA libraries.

Fluorescence *in situ* hybridization (FISH) of a cDNA clone to a metaphase 30 chromosomal spread can be used to provide a precise chromosomal location in one step. This technique can be used with cDNA as short as 50 or 60 bases. For a review of this technique, see

Verma et al., Human Chromosomes: a Manual of Basic Techniques, Pergamon Press, New York (1988).

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data 5 are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library). The relationship between genes and diseases that have been mapped to the same chromosomal region are then identified through linkage analysis (coinheritance of physically adjacent genes).

Next, it is necessary to determine the differences in the cDNA or genomic sequence 10 between affected and unaffected individuals. If a mutation is observed in some or all of the affected individuals but not in any normal individuals, then the mutation is likely to be the causative agent of the disease.

With current resolution of physical mapping and genetic mapping techniques, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 15 between 50 and 500 potential causative genes. (This assumes 1 megabase mapping resolution and one gene per 20 kb).

The polypeptides, their fragments or other derivatives, or analogs thereof, or cells expressing them can be used as an immunogen to produce antibodies thereto. These antibodies can be, for example, polyclonal or monoclonal antibodies. The present invention also includes 20 chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

Antibodies generated against the polypeptides corresponding to a sequence of the present invention can be obtained by direct injection of the polypeptides into an animal or by 25 administering the polypeptides to an animal, preferably a nonhuman. The antibody so obtained will then bind the polypeptides itself. In this manner, even a sequence encoding only a fragment of the polypeptides can be used to generate antibodies binding the whole native polypeptides. Such antibodies can then be used to isolate the polypeptide from tissue expressing that polypeptide.

30 For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma

technique (Kohler and Milstein, 1975, *Nature*, 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., 1983, *Immunology Today* 4:72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole, et al., 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96).

5 Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptide products of this invention. Also, transgenic mice may be used to express humanized antibodies to immunogenic polypeptide products of this invention.

10 The present invention will be further described with reference to the following examples; however, it is to be understood that the present invention is not limited to such examples. All parts or amounts, unless otherwise specified, are by weight.

In order to facilitate understanding of the following examples certain frequently occurring methods and/or terms will be described.

15 "Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

20 "Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 mg of plasmid or DNA fragment is used with about 2 units of enzyme in about 20 ml of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 25 50 mg of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37°C are ordinarily used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

30 Size separation of the cleaved fragments is performed using 8 percent polyacrylamide gel described by Goeddel, D. et al., *Nucleic Acids Res.*, 8:4057 (1980).

"Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A 5 synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

"Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Maniatis, T., et al., *Id.*, p. 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units of T4 DNA ligase ("ligase") per 0.5 mg of approximately equimolar amounts of the DNA fragments to be 10 ligated.

Unless otherwise stated, transformation was performed as described in the method of Graham, F. and Van der Eb, A., *Virology*, 52:456-457 (1973).

#### Example 1

15 Bacterial Expression and Purification of EEGF

The DNA sequence encoding the mature EEGF, ATCC # \_\_\_\_\_, is initially amplified using PCR oligonucleotide primers corresponding to the 5' sequences of the EEGF protein and the sequences 3' of the EEGF gene. The 5' oligonucleotide primer has the sequence 5' GACTGCATGCAGTGCACGAATGGCTTG3' (SEQ ID NO:3) contains an Sph I restriction enzyme site followed by 19 nucleotides of EEGF coding sequence starting from the presumed terminal amino acid. The 3' sequence 5' 20 GACTGGATCCGAATGGGTACTGCGACACATATATC 3' (SEQ ID NO:4) contains complementary sequences to a BamHI site (underlined) and is followed by 25 nucleotides of EEGF. The restriction enzyme sites correspond to the restriction enzyme sites on the bacterial expression vector pQE-70 (Qiagen, Inc. Chatsworth, CA). pQE-70 encodes antibiotic resistance (Amp<sup>r</sup>), a bacterial origin of replication (ori), an IPTG-regulatable promoter operator (P/O), a ribosome binding site (RBS), a 6-His tag and restriction enzyme sites. pQE-70 is then 25 digested with BamHI and SphI. The amplified sequences are ligated into pQE-70 and are inserted in frame with the sequence encoding for the histidine tag and the RBS. The ligation mixture is then used to transform E. coli strain M15/rep 4 (Qiagen, Inc.) by the procedure 30 described in Sambrook, J. et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring

Laboratory Press, (1989). M15/rep4 contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan'). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis. Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.<sup>600</sup>) of between 0.4 and 0.6. IPTG ("Isopropyl-B-D-thiogalacto pyranoside") is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression. Cells are grown an extra 3 to 4 hours. Cells are then harvested by centrifugation. The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl. After clarification, solubilized EEGF is purified from this solution by chromatography on a Nickel-Chelate column under conditions that allow for tight binding by proteins containing the 6-His tag (Hochuli, E. et al., J. Chromatography 411:177-184 (1984)). EEGF is eluted from the column in 6 molar guanidine HCl pH 5.0 and for the purpose of renaturation adjusted to 3 molar guanidine HCl, 100mM sodium phosphate, 10 mmolar glutathione (reduced) and 2 mmolar glutathione (oxidized). After incubation in this solution for 12 hours the protein is dialyzed to 10 mmolar sodium phosphate.

20

### Example 2

#### Cloning and expression of EEGF using the baculovirus expression system

The DNA sequence encoding the EEGF protein, ATCC # \_\_\_\_\_, is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the gene.

The primer sequences are as follows: 5'  
25      **GACTGGTACCGCCATCATGCCAGGAATAAAAGGATAC** 3' (SEQ ID NO:5), has a Asp718 restriction enzyme site (in bold) followed by 6 nucleotides resembling an efficient signal for the initiation of translation in eukaryotic cells (Kozak, M., J. Mol. Biol., 196:947-950 (1987) (the initiation codon for translation is "ATG") and 22 nucleotides corresponding to the 5' end of the full-length EEGF gene.  
30      The 3' primer 5' **GCATGGTACCGTCGGAGGCTCCAGCCGAGG** 3' (SEQ ID NO:6) contains the cleavage site for the restriction endonuclease Asn718 (bold) and 22

nucleotides complementary to the 3' end of the EEGF gene. The amplified sequences are isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment is then digested with the endonuclease Asp718 and then purified again on a 1% agarose gel. This fragment is designated F2.

5       The vector pA2 is used (modification of pVL941 vector, discussed below) for the expression of the EEGF protein using the baculovirus expression system (for review see: Summers, M.D. and Smith, G.E. 1987, A manual of methods for baculovirus vectors and insect cell culture procedures, Texas Agricultural Experimental Station Bulletin No. 1555). This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear  
10 polyhedrosis virus (AcMNPV) followed by the recognition sites for the restriction endonucleases. The polyadenylation site of the simian virus (SV)40 is used for efficient polyadenylation. For an easy selection of recombinant virus the beta-galactosidase gene from *E.coli* is inserted in the same orientation as the polyhedrin promoter followed by the polyadenylation signal of the polyhedrin gene. The polyhedrin sequences are flanked at both  
15 sides by viral sequences for the cell-mediated homologous recombination of co-transfected wild-type viral DNA. Many other baculovirus vectors could be used such as pAc373, pRG1, pVL941 and pAcIM1 (Luckow, V.A. and Summers, M.D., *Virology*, 170:31-39).

20       The plasmid is digested with the restriction enzyme Asp718 and then dephosphorylated using calf intestinal phosphatase by procedures known in the art. The DNA is then isolated from a 1% agarose gel using the commercially available kit ("Geneclean" BIO 101 Inc., La Jolla, Ca.). This vector DNA is designated V2.

25       Fragment F2 and the dephosphorylated plasmid V2 are ligated with T4 DNA ligase. *E.coli* HB101 cells are then transformed and bacteria identified that contained the plasmid (pBacEEGF) with the EEGF gene using the restriction enzyme Asp718. The sequence of the cloned fragment is confirmed by DNA sequencing.

30       5 mg of the plasmid pBacEEGF is co-transfected with 1.0 mg of a commercially available linearized baculovirus ("BaculoGoldÔ baculovirus DNA", Pharmingen, San Diego, CA.) using the lipofection method (Felgner et al. *Proc. Natl. Acad. Sci. USA*, 84:7413-7417 (1987)).

35       1mg of BaculoGoldÔ virus DNA and 5 mg of the plasmid pBacEEGF are mixed in a sterile well of a microtiter plate containing 50 ml of serum free Grace's medium (Life

Technologies Inc., Gaithersburg, MD). Afterwards 10 ml Lipofectin plus 90 ml Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to the Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is rocked back and forth to mix the newly added solution. The plate is then incubated for 5 hours at 27°C. After 5 hours the transfection solution is removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. The plate is put back into an incubator and cultivation continued at 27°C for four days.

After four days the supernatant is collected and a plaque assay performed similar as described by Summers and Smith (supra). As a modification an agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used which allows an easy isolation of blue stained plaques. (A detailed description of a "plaque assay" can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10).

Four days after the serial dilution, the virus is added to the cells and blue stained plaques are picked with the tip of an Eppendorf pipette. The agar containing the recombinant viruses is then resuspended in an Eppendorf tube containing 200 ml of Grace's medium. The agar is removed by a brief centrifugation and the supernatant containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then stored at 4°C.

Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus V-EEGF at a multiplicity of infection (MOI) of 2. Six hours later the medium is removed and replaced with SF900 II medium minus methionine and cysteine (Life Technologies Inc., Gaithersburg). 42 hours later 5 mCi of <sup>35</sup>S-methionine and 5 mCi <sup>35</sup>S cysteine (Amersham) are added. The cells are further incubated for 16 hours before they are harvested by centrifugation and the labelled proteins visualized by SDS-PAGE and autoradiography.

### Example 3

30 Expression of Recombinant EEGF in COS cells

The expression of plasmid, EEGF HA is derived from a vector pcDNA3/Amp (Invitrogen) containing: 1) SV40 origin of replication, 2) ampicillin resistance gene, 3) E.coli replication origin, 4) CMV promoter followed by a polylinker region, an SV40 intron and polyadenylation site. A DNA fragment encoding the entire EEGF precursor and a HA tag fused 5 in frame to its 3' end is cloned into the polylinker region of the vector, therefore, the recombinant protein expression is directed under the CMV promoter. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein as previously described (I. Wilson, H. Niman, R. Heighten, A. Cherenson, M. Connolly, and R. Lerner, 1984, Cell 37:767, 10 (1984)). The infusion of HA tag to the target protein allows easy detection of the recombinant protein with an antibody that recognizes the HA epitope.

The plasmid construction strategy is described as follows:

The DNA sequence encoding a preferred EEGF fragment, ATCC # 97285, is constructed by PCR using two primers: the 5' primer 5' GACTGGATCCGCCACCATGATGTGTGTTACCAAAATG 3' (SEQ ID NO:7) contains a 15 BamHI site (**in bold**) followed by 6 nucleotides resembling an efficient signal for the initiation of translation in eukaryotic cells and 22 nucleotides of EEGF coding sequence starting from the initiation codon; the 3' sequence 5' GACTTCTAGAGAATGGGTACTGCGACACATAT 3' (SEQ ID NO:8) contains complementary sequences to an XbaI site, 22 nucleotides of the EEGF gene followed by sequences encoding the HA tag. The pcDNA3/Amp vector contains 20 BamHI/XbaI cloning sites which bring the PCR insert in frame with the 3' HA tag followed by a stop codon. The PCR amplified DNA fragment and the vector, pcDNA3/Amp, are digested with BamHI and XbaI restriction enzyme and ligated. The ligation mixture is transformed into E. coli strain SURE (available from Stratagene Cloning Systems, La Jolla, CA 92037) the transformed culture is plated on ampicillin media plates and resistant colonies are selected. 25 Plasmid DNA is isolated from transformants and examined by restriction analysis for the presence of the correct fragment. For expression of the recombinant EEGF, COS cells are transfected with the expression vector by DEAE-DEXTRAN method (J. Sambrook, E. Fritsch, T. Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Laboratory Press, (1989)). The expression of the EEGF HA protein is detected by radiolabelling and immunoprecipitation 30 method (E. Harlow, D. Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, (1988)). Cells are labelled for 8 hours with <sup>35</sup>S-cysteine two days post

transfection. Culture media is then collected and cells are lysed with detergent (RIPA buffer (150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50mM Tris, pH 7.5) (Wilson, I. et al., Id. 37:767 (1984)). Both cell lysate and culture media are precipitated with an HA specific monoclonal antibody. Proteins precipitated are analyzed on 15% SDS-PAGE gels.

5

Example 4

Expression via Gene Therapy

Fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on 10 a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin, is added. This is then incubated at 37°C for approximately one week. At this 15 time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

pMV-7 (Kirschmeier, P.T. et al, DNA, 7:219-25 (1988) flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and 20 subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention is amplified using PCR primers which correspond to the 5' and 3' end sequences respectively. The 5' primer containing an EcoRI site and the 3' primer further includes a HindIII site. Equal quantities of the Moloney 25 murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is used to transform bacteria HB101, which are then plated onto agar-containing kanamycin for the purpose of confirming that the vector had the gene of interest properly inserted.

30 The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS),

penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells are transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

- 5        Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is  
10      removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his.

- 15      The engineered fibroblasts are then injected into the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads. The fibroblasts now produce the protein product.

Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, within the scope of the appended claims, the invention may be practiced otherwise than as particularly described.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5

(i) APPLICANT: OLSEN, HENRIK S.  
LI, HAODONG

10 (ii) TITLE OF INVENTION: EXTRACELLULAR EPIDERMAL GROWTH FACTOR  
LIKE PROTEIN

(iii) NUMBER OF SEQUENCES: 11

15

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
(B) STREET: 9410 KEY WEST AVENUE  
(C) CITY: ROCKVILLE  
(D) STATE: MD  
(E) COUNTRY: US  
20 (F) ZIP: 20850

25

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:

35

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BROOKES, ANDERS A.  
(B) REGISTRATION NUMBER: 36,373  
35 (C) REFERENCE/DOCKET NUMBER: PF224

40

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8509  
40 (B) TELEFAX: (301) 309-8512

## (2) INFORMATION FOR SEQ ID NO:1:

45

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1717 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
50 (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

55

## (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 211..1554

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 211..284

## 5 (ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 287..1554

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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15 CAGAGGAGGC CGACGTGCCG GAGCTCCTCC GGGGGTCCCG CCCGCGAGCT TTCTTCTCGC	180
CTTCGCATCT CCTCCTCGCG CGTCTTGGAC ATG CCA GGA ATA AAA AGG ATA CTC	234
Met Pro Gly Ile Lys Arg Ile Leu	
20 -25 -20	
ACT GTT ACC ATT CTG GCT CTC TGT CTT CCA AGC CCT GGG AAT GCA CAG	282
Thr Val Thr Ile Leu Ala Leu Cys Leu Pro Ser Pro Gly Asn Ala Gln	
-15 -10 -5	
25 GCA CAG TGC ACG AAT GGC TTT GAC CTG GAT CGC CAG TCA GGA CAG TGT	330
Ala Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys	
1 5 10 15	
30 TTA GAT ATT GAT GAA TGC CGA ACC ATC CCC GAG GCC TGC CGA GGA GAC	378
Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp	
20 25 30	
35 ATG ATG TGT GTT AAC CAA AAT GGC GGG TAT TTA TGC ATT CCC CGG ACA	426
Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr	
35 40 45	
40 AAC CCT GTG TAT CGA GGG CCC TAC TCG AAC CCC TAC TCG ACC CCC TAC	474
Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro Tyr	
50 55 60	
45 TCA GGT CCG TAC CCA GCA GCT GCC CCA CTC TCA GCT CCA AAC TAT	522
Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn Tyr	
65 70 75	
50 GAA AGC AAC CAA TGT GTG GAT GTG GAC GAG TGT GCA ACA GAT TCC CAC	618
Glu Ser Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His	
100 105 110	
55 CAG TGC AAC CCC ACC CAG ATC TGC ATC AAT ACT GAA GGC GGG TAC ACC	666
Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr	
115 120 125	

	TGC TCC TGC ACC GAC GGA TAT TGG CTT CTG GAA GGC CAG TGC TTA GAC Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp 130 135 140	714
5	ATT GAT GAA TGT CGC TAT GGT TAC TGC CAG CAG CTC TGT GCG AAT GTT Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val 145 150 155	762
10	CCT GGA TCC TAT TCT TGT ACA TGC AAC CCT GGT TTT ACC CTC AAT GAG Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Glu 160 165 170 175	810
15	GAT GGA AGG TCT TGC CAA GAT GTG AAC GAG TGT GCC ACC GAG AAC CCC Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Ala Thr Glu Asn Pro 180 185 190	858
20	TGC GTG CAA ACC TGC GTC AAC ACC TAC GGC TCT TTC ATC TGC CGC TGT Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys 195 200 205	906
25	GAC CCA GGA TAT GAA CTT GAG GAA GAT GGC GTT CAT TGC AGT GAT ATG Asp Pro Gly Tyr Glu Leu Glu Asp Gly Val His Cys Ser Asp Met 210 215 220	954
30	CAG CCC GGC ACA TAC TTC TGC TCC TGC CCT CCA GGC TAC ATC CTG CTG Gln Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Ile Leu Leu 240 245 250 255	1050
35	GAT GAC AAC CGA AGC TGC CAA GAC ATC AAC GAA TGT GAG CAC AGG AAC Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn 260 265 270	1098
40	CAC ACG TGC AAC CTG CAG CAG ACG TGC TAC AAT TTA CAA GGG GGC TTC His Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe 275 280 285	1146
45	AAA TGC ATC GAC CCC ATC CGC TGT GAG GAG CCT TAT CTG AGG ATC AGT Lys Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile Ser 290 295 300	1194
50	GAT AAC CGC TGT ATG TGT CCT GCT GAG AAC CCT GGC TGC AGA GAC CAG Asp Asn Arg Cys Met Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp Gln 305 310 315	1242
55	CCC TTT ACC ATC TTG TAC CGG GAC ATG GAC GTG GTG TCA GGA CGC TCC Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser 320 325 330 335	1290
	GTT CCC GCT GAC ATC TTC CAA ATG CAA GCC ACG ACC CGC TAC CCT GGG Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly 340 345 350	1338
	GCC TAT TAC ATT TTC CAG ATC AAA TCT GGG AAT GAG GGC AGA GAA TTT	1386

	Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe			
	355	360	365	
5	TAC ATG CGG CAA ACG GGC CCC ATC AGT GCC ACC CTG GTG ATG ACA CGC Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg		1434	
	370	375	380	
10	CCC ATC AAA GGG CCC CGG GAA ATC CAG CTG GAC TTG GAA ATG ATC ACT Pro Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu Glu Met Ile Thr		1482	
	385	390	395	
15	GTC AAC ACT GTC ATC AAC TTC AGA GGC AGC TCC GTG ATC CGA CTG CGG Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg		1530	
	400	405	410	415
20	ATA TAT GTG TCG CAG TAC CCA TTC TGAGCCTCGG GCTGGAGCCT CCGACGCTGC Ile Tyr Val Ser Gln Tyr Pro Phe		1584	
	420			
25	CTCTCATGG CACCAAGGGA CAGGAGAAGA GAGGAAATAA CAGAGAGAWT GAGAGCGAMA CAGACGTTAG GCATTTCTG CTGAACGTTT CCCCCGAAGAG TCAGNCCGA CTTCCGTACT CTCACCTGTA CTATTG		1644	
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			1717	
(2) INFORMATION FOR SEQ ID NO:2:				
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 448 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear			
35	(ii) MOLECULE TYPE: protein			
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:			
40	Met Pro Gly Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys -25 -20 -15 -10			
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45	Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr 10 15 20			
	Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly 25 30 35			
50	Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr 40 45 50 55			
	Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala 60 65 70			
55	Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile 75 80 85			

Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val  
 90 95 100

5 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys  
 105 110 115

Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp  
 120 125 130 135

10 Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr  
 140 145 150

Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys  
 15 155 160 165

Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val  
 170 175 180

20 Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr  
 185 190 195

Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu  
 200 205 210 215

25 Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe  
 220 225 230

Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser  
 30 235 240 245

Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp  
 250 255 260

35 Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr  
 265 270 275

Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys  
 280 285 290 295

40 Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala  
 300 305 310

Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp  
 45 315 320 325

Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met  
 330 335 340

50 Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys  
 345 350 355

Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile  
 360 365 370 375

55 Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile  
 380 385 390

Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg  
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5 Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe  
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10 (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

25 GACTGCATGC AGTGCACGAA TGGCTTTG 28

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 GACTGGATCC GAATGGGTAC TGGCACACAT ATATC 35

(2) INFORMATION FOR SEQ ID NO:5:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACTGGTACC GCCATCATGC CAGGAATAAA AAGGATAC

38

(2) INFORMATION FOR SEQ ID NO:6:

- 5       (i) SEQUENCE CHARACTERISTICS:  
          (A) LENGTH: 32 base pairs  
          (B) TYPE: nucleic acid  
          (C) STRANDEDNESS: single  
          (D) TOPOLOGY: linear

10      (ii) MOLECULE TYPE: DNA (genomic)

15      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCATGGTACC CGTCGGAGGC TCCAGCCCCGA GG

32

20      (2) INFORMATION FOR SEQ ID NO:7:

- 25       (i) SEQUENCE CHARACTERISTICS:  
          (A) LENGTH: 38 base pairs  
          (B) TYPE: nucleic acid  
          (C) STRANDEDNESS: single  
          (D) TOPOLOGY: linear

30      (ii) MOLECULE TYPE: DNA (genomic)

30      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

35      GACTGGATCC GCCACCATGA TGTGTGTTAA CCAAAATG

38

(2) INFORMATION FOR SEQ ID NO:8:

- 40       (i) SEQUENCE CHARACTERISTICS:  
          (A) LENGTH: 32 base pairs  
          (B) TYPE: nucleic acid  
          (C) STRANDEDNESS: single  
          (D) TOPOLOGY: linear

45      (ii) MOLECULE TYPE: DNA (genomic)

50      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACTTCTAGA GAATGGGTAC TGCGACACAT AT

32

(2) INFORMATION FOR SEQ ID NO:9:

- 55       (i) SEQUENCE CHARACTERISTICS:  
          (A) LENGTH: 368 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Val Ala Gly Pro Glu Met Gln Thr Gly Arg Asn Asn Phe Val Ile  
1 5 10 15

Arg Arg Asn Pro Ala Asp Pro Gln Arg Ile Pro Ser Asn Pro Ser His  
15 20 25 30

Arg Ile Gln Cys Ala Ala Gly Tyr Glu Gln Ser Glu His Asn Val Cys  
20 35 40 45

Gln Asp Ile Asp Glu Thr Ala Gly Thr His Asn Cys Arg Ala Asp Gln  
25 50 55 60

Val Cys Ile Asn Leu Arg Gly Ser Phe Ala Cys Gln Cys Pro Pro Gly  
25 65 70 75 80

Tyr Gln Lys Arg Gly Glu Gln Cys Val Asp Ile Asp Glu Cys Thr Ile  
30 85 90 95

Pro Pro Tyr Cys His Gln Arg Cys Val Asn Thr Pro Gly Ser Phe Tyr  
35 100 105 110

Cys Gln Cys Ser Pro Gly Phe Gln Leu Ala Ala Asn Asn Tyr Thr Cys  
40 115 120 125

Val Asp Ile Asn Glu Cys Asp Ala Ser Asn Gln Cys Ala Gln Gln Cys  
45 130 135 140

Tyr Asn Ile Leu Gly Ser Phe Ile Cys Gln Cys Asn Gln Gly Tyr Glu  
50 145 150 155 160

Leu Ser Ser Asp Arg Leu Asn Cys Glu Asp Ile Asp Glu Cys Arg Thr  
55 165 170 175

Ser Ser Tyr Leu Cys Gln Tyr Gln Cys Val Asn Glu Pro Gly Lys Phe  
60 180 185 190

Ser Cys Met Cys Pro Gln Gly Tyr Gln Val Val Arg Ser Arg Thr Cys  
65 195 200 205

Gln Asp Ile Asn Glu Cys Glu Thr Thr Asn Glu Cys Arg Glu Asp Glu  
70 210 215 220

Met Cys Trp Asn Tyr His Gly Gly Phe Arg Cys Tyr Pro Arg Asn Pro  
75 225 230 235 240

Cys Gln Asp Pro Tyr Ile Leu Thr Pro Glu Asn Arg Cys Val Cys Pro

	245	250	255	
	Val Ser Asn Ala Met Cys Arg Glu Leu Pro Gln Ser Ile Val Tyr Lys			
	260	265	270	
5	Tyr Met Ser Ile Arg Ser Asp Arg Ser Val Pro Ser Asp Ile Phe Gln			
	275	280	285	
	Ile Gln Ala Thr Thr Ile Tyr Ala Asn Thr Ile Asn Thr Phe Arg Ile			
10	290	295	300	
	Lys Ser Gly Asn Glu Asn Gly Glu Phe Tyr Leu Arg Gln Thr Ser Pro			
	305	310	315	320
15	Val Ser Ala Met Leu Val Leu Val Lys Ser Leu Gly Pro Arg Glu His			
	325	330	335	
	Ile Val Asp Leu Glu Met Leu Thr Val Ser Ser Ile Gly Thr Phe Arg			
	340	345	350	
20	Thr Ser Ser Val Leu Arg Leu Thr Ile Ile Val Gly Pro Phe Ser Phe			
	355	360	365	

## 25 (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 41 amino acids
  - (B) TYPE: amino acid
  - 30 (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

40	Thr Cys Gly Gln Gly Tyr Gln Leu Ser Ala Ala Lys Asp Gln Cys Glu			
	1	5	10	15
	Asp Ile Asp Glu Cys Gln His Arg His Leu Cys Ala His Gly Gln Cys			
	20	25	30	
45	Arg Asn Thr Glu Gly Ser Phe Gln Cys			
	35	40		

## (2) INFORMATION FOR SEQ ID NO:11:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 amino acids
  - (B) TYPE: amino acid
  - 55 (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

5       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

10      Ser Cys Ser Val Gly Phe Arg Leu Ser Val Asp Gly Arg Ser Cys Glu  
          1                   5                                   10                   15

15      Asp Ile Asn Glu Cys Ser Ser Pro Cys Ser Gln Glu Cys Ala Asn  
          20   25                   30

20      Val Tyr Gly Ser Glu Gly Phe Tyr Gln Cys  
          35    40

15

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a polynucleotide having at least a 95% identity to a member selected from the group consisting of:
  - (a) a polynucleotide encoding a polypeptide comprising an amino acid sequence set forth in SEQ ID NO:2 or the polypeptide encoding by ATCC Deposit No. \_\_\_\_\_;
  - (b) a polynucleotide encoding a polypeptide comprising an amino acid sequence set forth as residues 57 to 448 in SEQ ID NO:2 or as encoded by ATCC Deposit No. 97285;
  - (c) a polynucleotide encoding the mature EEGF polypeptide shown as residues 26 to 448 in SEQ ID NO:2 or as encoded by ATCC Deposit No. \_\_\_\_\_;
  - (d) a polynucleotide encoding the EGF-1 domain of EEGF shown as residues 112-153 of SEQ ID NO:2;
  - (e) a polynucleotide encoding the EGF-2 domain of EEGF shown as residues 154-190 of SEQ ID NO:2;
  - (f) a polynucleotide encoding the EGF-3 domain of EEGF shown as residues 191-230 of SEQ ID NO:2;
  - (g) a polynucleotide encoding the EGF-4 domain of EEGF shown as residues 231-271 of SEQ ID NO:2;
  - (h) a polynucleotide encoding the EGF-5 domain of EEGF shown as residues 272-314; and
  - (i) a polynucleotide which is complementary to the polynucleotide of (a), (b), (c), (d), (e), (f), (g) or (h).
2. The polynucleotide of Claim 1 wherein the polynucleotide is DNA.
3. The polynucleotide of Claim 1 wherein the polynucleotide is RNA.
4. The polynucleotide of claim 1 comprising nucleotide 286 to nucleotide 1554 of SEQ ID NO:1.

5. The polynucleotide of claim 1 comprising nucleotide 211 to nucleotide 1554 of SEQ ID NO:1.
6. A vector comprising the DNA of Claim 2.
7. A host cell comprising the vector of Claim 6.
8. A process for producing a polypeptide comprising: expressing from the host cell of Claim 7 the polypeptide encoded by said DNA.
9. A process for producing cells capable of expressing a polypeptide comprising genetically engineering cells with the vector of Claim 6.
10. A polypeptide comprising an amino acid sequence which is at least 95% identical to an amino acid sequence selected from the group comprising:
  - (a) the amino acid sequence of the complete EEGF polypeptide set forth in SEQ ID NO:2, or the amino acid sequence of the polypeptide encoded by the cDNA contained in ATCC Deposit No. \_\_\_\_\_;
  - (b) the amino acid sequence of the EEGF polypeptide set forth in SEQ ID NO:2 as residues 57 to 448, or the amino acid sequence of the polypeptide encoded by the cDNA contained in ATCC Deposit No. 97285;
  - (c) the amino acid sequence of the mature EEGF polypeptide set forth as residues 26 to 448 in SEQ ID NO:2, or the amino acid sequence of the mature EEGF polypeptide encoded by ATCC Deposit No. \_\_\_\_\_;
  - (d) the amino acid sequence of the EGF-1 domain of EEGF shown as residues 112-153 in SEQ ID NO:2;
  - (e) the amino acid sequence of the EGF-2 domain of EEGF shown as residues 154-190 in SEQ ID NO:2;
  - (f) the amino acid sequence of the EGF-3 domain of EEGF shown as residues 191-230 in SEQ ID NO:2;

(g) the amino acid sequence of the EGF-4 domain of EEGF shown as residues 231-271 in SEQ ID NO:2; and  
(h) the amino acid sequence of the EGF-5 domain of EEGF shown as residues 272-314 in SEQ ID NO:2.

11. An antibody against the polypeptide of claim 10.

12. An antagonist for the polypeptide of claim 10.

13. A method for the treatment of a patient having need of EEGF comprising: administering to the patient a therapeutically effective amount of the polypeptide of claim 10.

14. A method for the treatment of a patient having need to inhibit EEGF comprising: administering to the patient a therapeutically effective amount of the antagonist of Claim 12.

15. The method of Claim 14 wherein said therapeutically effective amount of the polypeptide is administered by providing to the patient DNA encoding said polypeptide and expressing said polypeptide *in vivo*.

16. A process for identifying compounds active as antagonists to the polypeptide of Claim 10 comprising: contacting a reaction mixture containing a cell type which expresses the EEGF receptor and a compound to be screened; and detecting the absence of a signal generated from said receptor after binding of said compound to identify if the compound is an effective antagonist.

17. A process for diagnosing a disease or a susceptibility to a disease comprising: determining a mutation in the polynucleotide of claim 1.

18. A diagnostic process comprising: analyzing for the presence of the polypeptide of Claim 10 in a sample.

Fig. 1A

1	AACCAGGTGCTTGCCTGAGGGCTCTGCAGTGGCTGGGAGGACCCGGCGCTCTCCCG	60
61	TGTCCCTCTCCACGACTCGCTCGGCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCC	120
121	CAGAGGAGGCCGACGTGCCGAGCTCCTCCGGGGTCCGCCGAGCTTCCTCTCGC	180
181	CTTCGCATCTCCTCCCGCGTCTGGACATGCCAGGAATAAAAGGATACTCACTGTT MetProGlyIleLysArgIleLeuThrVal <u>M P G I K R I L T V</u>	240
241	ACCATTCTGGCTCTGTCTTCCAAGCCCTGGGAATGCACAGGCACAGTGCACGAATGGC ThrIleLeuAlaLeuCysLeuProSerProGlyAsnAlaGlnAlaGlnCysThrAsnGly <u>T I L A L C L P S P G N A O A Q C T N G</u>	300
301	TTTGACCTGGATGCCAGTCAGGACAGTGTAGATATTGATGAATGCCAACCATCCCC PheAspLeuAspArgGlnSerGlyGlnCysLeuAspIleAspGluCysArgThrIlePro <u>F D L D R Q S G Q C L D I D E C R T I P</u>	360
361	GAGGCCTGCCGAGGAGACATGATGTGTAAACAAAATGGGGTATTTATGCATTCCC GluAlaCysArgGlyAspMetMetCysValAsnGlnAsnGlyTyrLeuCysIlePro <u>E A C R G D M M C V N Q N G G Y L C I P</u>	420
421	CGGACAAACCTGTGTATCGAGGGCCCTACTCGAACCCCTACTCGACCCCTACTCAGGT ArgThrAsnProValTyrArgGlyProTyrSerAsnProTyrSerThrProTyrSerGly <u>R T N P V Y R G P Y S N P Y S T P Y S G</u>	480
481	CCGTACCCAGCAGCTGCCCACTCTCAGCTCCAAACTATCCCACGATCTCCAGGCCT ProTyrProAlaAlaAlaProProLeuSerAlaProAsnTyrProThrIleSerArgPro <u>P Y P A A A P P L S A P N Y P T I S R P</u>	540

**Fig. 1B**

**Fig. 1C**

1021 TGCTCCTGCCCTCCAGGCTACATCTGCTGGATGACAACCGAAGCTGCCAAGACATCAAC  
 CysSerCysProProGlyTyrIleLeuLeuAspAspAsnArgSerCysGlnAspIleAsn  
 C S C P P G Y I L L D D N R S C Q D I N  
 | | \*\*\*\*\*  
 1081 GAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGCTACAATTACAAGGG  
 GluCysGluHisArgAsnHisThrCysAsnLeuGlnGlnThrCysTyrAsnLeuGlnGly  
 E C E H R N H T C N L Q Q T C Y N L Q G  
 \* \* \* \* \* EGF-5 \* \* \* \* \*  
 1141 GGCTTCAAATGCATCGACCCCCATCCGCTGTGAGGAGCCTTATCTGAGGATCAGTGATAAC  
 GlyPheLysCysIleAspProIleArgCysGluGluProTyrLeuArgIleSerAspAsn  
 G F K C I D P I R C E E P Y L R I S D N  
 \* \* \* \* \* |  
 1201 CGCTGTATGTGTCCTGCTGAGAACCCCTGGCTGCAGAGACCAGGCCCTTACCATTTGTAC  
 ArgCysMetCysProAlaGluAsnProGlyCysArgAspGlnProPheThrIleLeuTyr  
 R C M C P A E N P G C R D Q P F T I L Y  
 1261 CGGGACATGGACGTGGTGTCAAGGACGCTCCGTTCCCGCTGACATCTTCAAATGCAAGCC  
 ArgAspMetAspValValSerGlyArgSerValProAlaAspIlePheGlnMetGlnAla  
 R D M D V V S G R S V P A D I F Q M Q A  
 1321 ACGACCCGCTACCCCTGGGGCTATTACATTTCCAGATCAAATCTGGGAATGAGGGCAGA  
 ThrThrArgTyrProGlyAlaTyrTyrIlePheGlnIleLysSerGlyAsnGluGlyArg  
 T T R Y P G A Y Y I F Q I K S G N E G R  
 1381 GAATTTACATGCGGAAACGGGCCCATCAGTGCCACCCCTGGTGTGACACGCCCATC  
 GluPheTyrMetArgGlnThrGlyProIleSerAlaThrLeuValMetThrArgProIle  
 E F Y M R Q T G P I S A T L V M T R P I  
 1441 AAAGGGCCCCGGGAAATCCAGCTGGACTTGGAAATGATCACTGTCAACACTGTCAAC  
 LysGlyProArgGluIleGlnLeuAspLeuGluMetIleThrValAsnThrValIleAsn  
 K G P R E I Q L D L E M I T V N T V I N

**Fig. 1D**

1501      TTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTCGCAGTACCCATTCTGAGCC      1560  
-----+-----+-----+-----+-----+-----+  
PheArgGlySerSerValIleArgLeuArgIleTyrValSerGlnTyrProPheEnd  
F R G S S V I R L R I Y V S Q Y P F \*  
  
1561      TCGGGCTGGAGCCTCCGACGCTGCCCTCTCATTGGCACCAAGGGACAGGAGAAGAGAGGAA      1620  
-----+-----+-----+-----+-----+-----+  
  
1621      ATAACAGAGAGAWTGAGAGCGAMACAGACGTTAGGCATTCTGCTAACGTTCCCCGA      1680  
-----+-----+-----+-----+-----+-----+  
  
1681      AGAGTCAGNCCCACCTCCTGACTCTCACCTGTACTATTG      1720  
-----+-----+-----+-----+

**Fig. 2**

AVAGPEMQTGRNNFVIRRNPADPQRIPSNPSPHRIQCAAGYEQSEHNVCQDIDECTAGTHN  
|:::| |::| |::| |::| |::| |::|

GPYSNPYSTPYSGPYAAPPLSAFPNYPTISRPLICRGYQMDESNQCVDVDECATDSHQ  
|:::| |::| |::| |::| |::| |::| |::|

CRADQVCINLRGSFACQCPPGYQKRG EQCVDIDECTIPPYCHQRCVNTPGSPYCQCSPGF  
|:::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

QLAANNYTCVDINECDASNQCAQQCYNILGSFICQCNCQGYELSSDRLNCEDEICRTSSY  
|:::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

TLINEGRSCQDVNECATENPCVQTCVNTYGSFICRCDFGTLEEDGVHCSDMDECFSSET

LCQYOCVNNEPGKFSMCPQGYQVV-RSRTCQDINECE-TTNECREDEMWCWNYHGGFRCPY  
|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

LCQHECVNQPGTYFCSCPQGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCID

RNPQDQPYILTPENRVCVPVSAMCRELPOSIVVKYMSIRSDRSVPSDIFQIQATTIYAN  
|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

PIRCEEPYLRISENRCMCPAENPGCRDQPFTILYRIMDVVSGRSVPADIFQMQATTTRYPG

TINTFRIGSGNENGEGFYLRQTSFVSAVLVLUKSLSGPREHIVDLEMUTVSSIGTFRTSSV  
|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

AYYIFQIKSGNEGREFYMRQGPISATLVMTRPIKGPREIQLDLEMITVTNTVINFRGSSV

LRLTIIIVGPFSP  
|::| |::|  
IRLRIYVSQYPP

Fig. 3

1	I	C	R	F	G	Y	O	M	D	E	S	N	-	Q	C	V	D	V	D	E	C	A	T	D	S	H	Q	C	N	P		
1	S	C	T	D	G	Y	W	L	L	E	G	-	-	Q	C	L	D	I	D	E	C	R	Y	G	Y	-	C	-	EEGF	EGF-1		
1	T	C	N	P	G	F	T	L	N	E	D	G	R	S	C	S	D	V	N	E	C	A	T	-	E	N	P	C	V	-	EEGF	EGF-2
1	R	C	D	P	G	Y	E	L	E	D	G	V	H	C	S	D	M	D	E	C	S	F	S	E	F	L	C	-	EEGF	EGF-3		
1	S	C	P	P	G	Y	I	L	L	D	D	N	R	S	C	Q	D	I	N	E	C	E	H	R	N	H	T	C	N	L	EEGF	EGF-4
1	T	C	G	Q	G	Y	O	L	S	A	K	D	Q	C	E	D	I	D	E	C	Q	H	R	-	H	L	C	A	-	TGF-B1	EGF	
1	S	C	S	V	G	F	R	L	S	V	D	G	R	S	C	E	D	I	N	E	S	S	P	C	S	-	-	FBL	EGF			
30	T	Q	I	I	C	I	N	-	-	T	E	G	G	Y	T	C	-	-	-	-	-	-	-	-	-	-	-	-	-	EEGF	EGF-1	
25	Q	Q	L	C	A	N	V	P	G	S	-	-	-	-	-	Y	S	C	-	-	-	-	-	-	-	-	-	-	-	EEGF	EGF-2	
29	-	Q	T	C	V	N	T	Y	G	S	-	-	-	-	-	F	I	C	-	-	-	-	-	-	-	-	-	-	-	EEGF	EGF-3	
29	Q	H	E	C	V	N	Q	P	G	T	-	-	-	-	-	Y	F	-	C	-	-	-	-	-	-	-	-	-	-	EEGF	EGF-4	
31	Q	Q	T	C	Y	N	L	Q	G	G	-	-	-	-	-	F	K	C	-	-	-	-	-	-	-	-	-	-	-	EEGF	EGF-5	
29	H	G	Q	C	R	N	-	-	T	E	G	S	F	Q	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TGF-B1	EGF	
28	-	Q	E	C	A	N	V	Y	G	S	E	G	F	Y	Q	C	-	-	-	-	-	-	-	-	-	-	-	-	-	FBL	EGF	

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description  
on page 3, line 25

## B. IDENTIFICATION OF DEPOSIT

Further deposits are identified on an additional sheet 

Name of depositary institution

American Type Culture Collection

Address of depositary institution (*including postal code and country*)12301 Parklawn Drive  
Rockville, Maryland 20852  
United States of AmericaDate of deposit September 18, 1997

Accession Number

209278C. ADDITIONAL INDICATIONS (*leave blank if not applicable*)This information is continued on an additional sheet 

## EUROPE

In respect of those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (*if the indications are not for all designated States*)E. SEPARATE FURNISHING OF INDICATIONS (*leave blank if not applicable*)

The indications listed below will be submitted to the International Bureau later (*specify the general nature of the indications e.g. "Accession Number of Deposit"*)

For receiving Office use only

 This sheet was received with the international application

For International Bureau use only

 This sheet was received by the International Bureau on:

8 January 1998

Authorized officer

Authorized officer

### SINGAPORE

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for international publication of the application.

### NORWAY

The applicant hereby requests that, until the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Norwegian Patent office or any person approved by the applicant in the individual case.

### AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

### FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Registration), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

### ICELAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

page 2

#### DENMARK

The applicant hereby request that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent office or any person approved by the applicant in the individual case.

#### SWEDEN

The applicant hereby request that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent office or any person approved by the applicant in the individual case.

#### UNITED KINGDOM

The applicant hereby request that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for international publication of the application.

#### NETHERLANDS

The applicant hereby request that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

**INTERNATIONAL SEARCH REPORT**

Int'l. Appl. No PCT/US 97/06020
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<b>A. CLASSIFICATION OF SUBJECT MATTER</b>
IPC 6 C12N15/12 C07K14/485 C07K16/22 G01N33/50 G01N33/53 A61K31/70 A61K38/18 A61K48/00 C12Q1/68 C12N1/21 C12N5/10 C12N15/86 //((C12N1/21,C12R1:19)

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)  
IPC 6 C12N C07K G01N A61K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	EMBL Database entry Hs726155 Accession number H17726; 4. July 1995 HILLIER L. ET AL.: 'The WashU-Merck EST Project.' XP002036779 see abstract --- EMBL Database entry Hs599207 Accession number H54599; 22.September 1995 HILLIER L. ET AL.: The WashU-Merck EST Project.' XP002036780 see abstract ---	1-11
A	---	1-11

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

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Date of the actual completion of the international search  9 December 1997	Date of mailing of the international search report  20.01.1998
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**INTERNATIONAL SEARCH REPORT**

International Application No
PCT/US 97/06020

**C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>LECKA-CZERNIK B. ET AL.: "An overexpressed gene transcript in senescent and quiescent human fibroblasts encoding a novel protein in the epidermal growth-factor-like repeat family stimulates DNA synthesis."</p> <p>MOLECULAR AND CELLULAR BIOLOGY, vol. 15, no. 1, 1995, pages 120-128, XP002036980 cited in the application see the whole document</p> <p>---</p>	1-11
A	<p>DE 39 02 157 A (ONCOGEN) 27 July 1989 cited in the application see the whole document</p> <p>-----</p>	1-18

**INTERNATIONAL SEARCH REPORT**

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